SEQUENCE LISTING

<110> Daniel E. Afar
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      Douglas C. Saffran
      Stephen C. Mitchell

<120> NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
   EXPRESSED IN HUMAN CANCERS AND USES THEREOF

<130> 129.17-US-I1

<140> 09/455,486
<141> 1999-12-06

<150> 09/323,873
<151> 1999-06-01

<160> 34

<170> FastSEQ for Windows Version 4.0

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    Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys
      1               5                  10                  15

atg aag cct agg aga aat tta gaa gaa gac gat tat ttg cat aag gac       156
Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
                  20              25                  30

acg gga gag acc agc atg cta aaa aga cct gtg ctt ttg cat ttg cac       204
Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
              35                  40                  45

caa aca gcc cat gct gat gaa ttt gac tgc cct tca gaa ctt cag cac       252
Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
          50                  55                  60

aca cag gaa ctc ttt cca cag tgg cac ttg cca att aaa ata gct gct       300
Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
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att ata gca tct ctg act ttt ctt tac act ctt ctg agg gaa gta att       348
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1

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Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
 80              85              90                  95

cac cct tta gca act tcc cat caa caa tat ttt tat aaa att cca atc     396
His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile
            100             105                 110

ctg gtc atc aac aaa gtc ttg cca atg gtt tcc atc act ctc ttg gca     444
Leu Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala
            115             120                 125

ttg gtt tac ctg cca ggt gtg ata gca gca att gtc caa ctt cat aat     492
Leu Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn
            130             135                 140

gga acc aag tat aag aag ttt cca cat tgg ttg gat aag tgg atg tta     540
Gly Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu
            145             150                 155

aca aga aag cag ttt ggg ctt ctc agt ttc ttt ttt gct gta ctg cat     588
Thr Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His
160             165             170                 175

gca att tat agt ctg tct tac cca atg agg cga tcc tac aga tac aag     636
Ala Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys
            180             185                 190

ttg cta aac tgg gca tat caa cag gtc caa caa aat aaa gaa gat gcc     684
Leu Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala
            195             200                 205

tgg att gag cat gat gtt tgg aga atg gag att tat gtg tct ctg gga     732
Trp Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly
            210             215                 220

att gtg gga ttg gca ata ctg gct ctg ttg gct gtg aca tct att cca     780
Ile Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro
            225             230                 235

tct gtg agt gac tct ttg aca tgg aga gaa ttt cac tat att cag agc     828
Ser Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser
240             245             250                 255

aag cta gga att gtt tcc ctt cta ctg ggc aca ata cac gca ttg att     876
Lys Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile
            260             265                 270

ttt gcc tgg aat aag tgg ata gat ata aaa caa ttt gta tgg tat aca     924
Phe Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr
            275             280                 285

cct cca act ttt atg ata gct gtt ttc ctt cca att gtt gtc ctg ata     972
Pro Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile
            290             295                 300

ttt aaa agc ata cta ttc ctg cca tgc ttg agg aag aag ata ctg aag    1020
Phe Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys
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2

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att aga cat ggt tgg gaa gac gtc acc aaa att aac aaa act gag ata      1068
Ile Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile
320                 325                 330                 335

tgt tcc cag ttg tag aattactgtt tacacacatt tttgttcaat attgatatat     1123
Cys Ser Gln Leu  *


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<213> Homo sapiens

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Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
        35                  40                  45
Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
    50                  55                  60
Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
65                  70                  75                  80
Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His
                85                  90                  95
Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
            100                 105                 110
Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
            115                 120                 125
Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
    130                 135                 140
Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
145                 150                 155                 160
Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
                165                 170                 175
Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
            180                 185                 190
Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
            195                 200                 205
Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
    210                 215                 220
Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
225                 230                 235                 240
Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
                245                 250                 255
Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
            260                 265                 270
Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
            275                 280                 285
Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
    290                 295                 300
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Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
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Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
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Ser Gln Leu

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<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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accaagaaga actttggaaa atgaagccta ggagaaattt agaagaagac gattatttgc   180
ataaggacac gggagagacc agcatgctaa aaagacctgt gcttttgcat ttgcaccaaa   240
cagcccatgc tgatgaattt gactgcccct cagaacttca gcacacacag gaactctttc   300
cacagtggca cttgccaatt aaaatagctg ctattatagc atctctgact tttctttaca   360
ctcttctgag ggaagtaatt caccccttag caacttccca tcaacaatat ttttataaaa   420
ttccaatcct ggtcatcaac aaagtcttgc caatggtttc catcactctc ttggcattgg   480
tttacctgcc aggtgtgata gcagcaattg tccaacttca taatggaacc aagtataaga   540
agtttccaca ttggttggat aagtggatgt aacaagaaa gcagtttggg cttctcagtt   600
tcttttttgc tgtactgcat gcaatttata gtctgtctta cccaatgagg cgatcctaca   660
gatacaagtt gctaaactgg gcatatcaac aggtccaaca aaataaagaa gatgcctgga   720
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tactggctct gttggctgtg acatctattc catctgtgag tgactctttg acatggagag   840
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tgtgtttatg atatagaata tgttgacttt accccataaa aaataacaaa tgttttttcaa   960
cagcaaagat cttatacttg ttccaattaa taatgtgctc tcctgttgtt ttccctattg   1020
cttctaatta ggacaagtgt ttcctagaca taaataaaag gcattaaaat attctttgtt   1080
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4

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agtaacctag aaatgtttca cttaaaatct gagaactggt tacactacaa gttaccttgg      2340
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cccctggctg ttcgcgatcc agcttgggta ggcggggaag cagctggagt gcgaccgcca      180
cggcagccac cctgcaaccg ccagtcggag gtgcagtccg taggccctgg cccccgggtg      240
ggcccttggg gagtcggcgc cgctcccgag gagctgcaag gctcgcccct gcccggcgtg      300
gagggcgcgg ggggcgcgga ggatattctt ggtgatcttg aagtgtccg tatc atg      357
                                                            Met
                                                             1


gaa tca atc tct atg atg gga agc cct aag agc ctt agt gaa act tgt      405
Glu Ser Ile Ser Met Met Gly Ser Pro Lys Ser Leu Ser Glu Thr Cys
            5               10                  15


tta cct aat ggc ata aat ggt atc aaa gat gca agg aag gtc act gta      453
Leu Pro Asn Gly Ile Asn Gly Ile Lys Asp Ala Arg Lys Val Thr Val
        20                  25                  30


ggt gtg att gga agt gga gat ttt gcc aaa tcc ttg acc att cga ctt      501
Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg Leu
    35                  40                  45
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att aga tgc ggc tat cat gtg gtc ata gga agt aga aat cct aag ttt          549
Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys Phe
50                  55                  60                  65

gct tct gaa ttt ttt cct cat gtg gta gat gtc act cat cat gaa gat          597
Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu Asp
                    70                  75                  80

gct ctc aca aaa aca aat ata ata ttt gtt gct ata cac aga gaa cat          645
Ala Leu Thr Lys Thr Asn Ile Ile Phe Val Ala Ile His Arg Glu His
                85                  90                  95

tat acc tcc ctg tgg gac ctg aga cat ctg ctt gtg ggt aaa atc ctg          693
Tyr Thr Ser Leu Trp Asp Leu Arg His Leu Leu Val Gly Lys Ile Leu
            100                 105                 110

att gat gtg agc aat aac atg agg ata aac cag tac cca gaa tcc aat          741
Ile Asp Val Ser Asn Asn Met Arg Ile Asn Gln Tyr Pro Glu Ser Asn
        115                 120                 125

gct gaa tat ttg gct tca tta ttc cca gat tct ttg att gtc aaa gga          789
Ala Glu Tyr Leu Ala Ser Leu Phe Pro Asp Ser Leu Ile Val Lys Gly
130                 135                 140                 145

ttt aat gtt gtc tca gct tgg gca ctt cag tta gga cct aag gat gcc          837
Phe Asn Val Val Ser Ala Trp Ala Leu Gln Leu Gly Pro Lys Asp Ala
                150                 155                 160

agc cgg cag gtt tat ata tgc agc aac aat att caa gcg cga caa cag          885
Ser Arg Gln Val Tyr Ile Cys Ser Asn Asn Ile Gln Ala Arg Gln Gln
                165                 170                 175

gtt att gaa ctt gcc cgc cag ttg aat ttc att ccc att gac ttg gga          933
Val Ile Glu Leu Ala Arg Gln Leu Asn Phe Ile Pro Ile Asp Leu Gly
            180                 185                 190

tcc tta tca tca gcc aga gag att gaa aat tta ccc cta cga ctc ttt          981
Ser Leu Ser Ser Ala Arg Glu Ile Glu Asn Leu Pro Leu Arg Leu Phe
        195                 200                 205

act ctc tgg aga ggg cca gtg gtg gta gct ata agc ttg gcc aca ttt         1029
Thr Leu Trp Arg Gly Pro Val Val Val Ala Ile Ser Leu Ala Thr Phe
210                 215                 220                 225

ttt ttc ctt tat tcc ttt gtc aga gat gtg att cat cca tat gct aga         1077
Phe Phe Leu Tyr Ser Phe Val Arg Asp Val Ile His Pro Tyr Ala Arg
                230                 235                 240

aac caa cag agt gac ttt tac aaa att cct ata gag att gtg aat aaa         1125
Asn Gln Gln Ser Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys
                245                 250                 255

acc tta cct ata gtt gcc att act ttg ctc tcc cta gta tac ctt gca         1173
Thr Leu Pro Ile Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala
            260                 265                 270
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6

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ggt ctt ctg gca gct gct tat caa ctt tat tac ggc acc aag tat agg        1221
Gly Leu Leu Ala Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr Arg
    275             280             285

aga ttt cca cct tgg ttg gaa acc tgg tta cag tgt aga aaa cag ctt        1269
Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln Leu
290             295             300             305

gga tta cta agt ttt ttc ttc gct atg gtc cat gtt gcc tac agc ctc        1317
Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val Ala Tyr Ser Leu
            310             315             320

tgc tta ccg atg aga agg tca gag aga tat ttg ttt ctc aac atg gct        1365
Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met Ala
            325             330             335

tat cag cag gtt cat gca aat att gaa aac tct tgg aat gag gaa gaa        1413
Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu
            340             345             350

gtt tgg aga att gaa atg tat atc tcc ttt ggc ata atg agc ctt ggc        1461
Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly
    355             360             365

tta ctt tcc ctc ctg gca gtc act tct atc cct tca gtg agc aat gct        1509
Leu Leu Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala
370             375             380             385

tta aac tgg aga gaa ttc agt ttt att cag tct aca ctt gga tat gtc       .1557
Leu Asn Trp Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val
            390             395             400

gct ctg ctc ata agt act ttc cat gtt tta att tat gga tgg aaa cga        1605
Ala Leu Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys Arg
            405             410             415

gct ttt gag gaa gag tac tac aga ttt tat aca cca cca aac ttt gtt        1653
Ala Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe Val
            420             425             430

ctt gct ctt gtt ttg ccc tca att gta att ctg gat ctt ttg cag ctt        1701
Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Asp Leu Leu Gln Leu
    435             440             445

tgc aga tac cca gac tga gctggaactg gaatttgtct tcctattgac             1749
Cys Arg Tyr Pro Asp  *
450

tctacttctt taaaagcggc tgcccattac attcctcagc tgtccttgca gttaggtgta    1809
catgtgactg agtgttggcc agtgagatga agtctcctca aaggaaggca gcatgtgtcc    1869
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actacttccc tacttccact gcttttcctg catttaagcc attgtaaatc tgggtgtgtt    2049
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gcaattcaca ttaaaattga ttttccattg tcaattagtt atactcattt cctgccttg    2229
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7

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ttggtaatta ctaaaactct gtaatctcca aaatattgct atcaaattac acaccatgtt    2349
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ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa                      2453
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<212> PRT
<213> Homo sapiens

<400> 6

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Val Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg
        35                  40                  45
Leu Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys
    50                  55                  60
Phe Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu
65                  70                  75                  80
Asp Ala Leu Thr Lys Thr Asn Ile Ile Phe Val Ala Ile His Arg Glu
                85                  90                  95
His Tyr Thr Ser Leu Trp Asp Leu Arg His Leu Leu Val Gly Lys Ile
            100                 105                 110
Leu Ile Asp Val Ser Asn Asn Met Arg Ile Asn Gln Tyr Pro Glu Ser
            115                 120                 125
Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Asp Ser Leu Ile Val Lys
    130                 135                 140
Gly Phe Asn Val Val Ser Ala Trp Ala Leu Gln Leu Gly Pro Lys Asp
145                 150                 155                 160
Ala Ser Arg Gln Val Tyr Ile Cys Ser Asn Asn Ile Gln Ala Arg Gln
                165                 170                 175
Gln Val Ile Glu Leu Ala Arg Gln Leu Asn Phe Ile Pro Ile Asp Leu
            180                 185                 190
Gly Ser Leu Ser Ser Ala Arg Glu Ile Glu Asn Leu Pro Leu Arg Leu
        195                 200                 205
Phe Thr Leu Trp Arg Gly Pro Val Val Val Ala Ile Ser Leu Ala Thr
    210                 215                 220
Phe Phe Phe Leu Tyr Ser Phe Val Arg Asp Val Ile His Pro Tyr Ala
225                 230                 235                 240
Arg Asn Gln Gln Ser Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn
                245                 250                 255
Lys Thr Leu Pro Ile Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu
                260                 265                 270
Ala Gly Leu Leu Ala Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr
            275                 280                 285
Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln
    290                 295                 300
Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val Ala Tyr Ser
305                 310                 315                 320
Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met
                325                 330                 335
Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu
            340                 345                 350
Glu Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu
        355                 360                 365
Gly Leu Leu Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn
```

8

```
              370                      375                      380
Ala Leu Asn Trp Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr
385                      390                      395                      400
Val Ala Leu Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys
                        405                      410                      415
Arg Ala Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe
                420                      425                      430
Val Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Asp Leu Leu Gln
            435                      440                      445
Leu Cys Arg Tyr Pro Asp
            450
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<210> 7
<211> 4429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (85)...(1464)

<400> 7

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cgaaacttcc ctctacccgc ccggcccgcg gcgcgcaccg ttggcgctgg acgcttcctc        60
cttggaagcg cctctccctc agtt atg gag aaa act tgt ata gat gca ctt        111
                           Met Glu Lys Thr Cys Ile Asp Ala Leu
                           1               5

cct ctt act atg aat tct tca gaa aag caa gag act gta tgt att ttt        159
Pro Leu Thr Met Asn Ser Ser Glu Lys Gln Glu Thr Val Cys Ile Phe
 10              15                      20                      25

gga act ggt gat ttt gga aga tca ctg gga ttg aaa atg ctc cag tgt        207
Gly Thr Gly Asp Phe Gly Arg Ser Leu Gly Leu Lys Met Leu Gln Cys
                30                      35                      40

ggt tat tct gtt gtt ttt gga agt cga aac ccc cag aag acc acc cta        255
Gly Tyr Ser Val Val Phe Gly Ser Arg Asn Pro Gln Lys Thr Thr Leu
            45                      50                      55

ctg ccc agt ggt gca gaa gtc ttg agc tat tca gaa gca gcc aag aag        303
Leu Pro Ser Gly Ala Glu Val Leu Ser Tyr Ser Glu Ala Ala Lys Lys
        60                      65                      70

tct ggc atc ata atc ata gca atc cac aga gag cat tat gat ttt ctc        351
Ser Gly Ile Ile Ile Ile Ala Ile His Arg Glu His Tyr Asp Phe Leu
    75                      80                      85

aca gaa tta act gag gtt ctc aat gga aaa ata ttg gta gac atc agc        399
Thr Glu Leu Thr Glu Val Leu Asn Gly Lys Ile Leu Val Asp Ile Ser
 90                      95                      100                     105

aac aac ctc aaa atc aat caa tat cca gaa tct aat gca gag tac ctt        447
Asn Asn Leu Lys Ile Asn Gln Tyr Pro Glu Ser Asn Ala Glu Tyr Leu
                110                     115                     120

gct cat ttg gtg cca gga gcc cac gtg gta aaa gca ttt aac acc atc        495
Ala His Leu Val Pro Gly Ala His Val Val Lys Ala Phe Asn Thr Ile
```

9

```
tca gcc tgg gct ctc cag tca gga gca ctg gat gca agt cgg cag gtg          543
Ser Ala Trp Ala Leu Gln Ser Gly Ala Leu Asp Ala Ser Arg Gln Val
        140                 145                 150

ttt gtg tgt gga aat gac agc aaa gcc aag caa aga gtg atg gat att          591
Phe Val Cys Gly Asn Asp Ser Lys Ala Lys Gln Arg Val Met Asp Ile
        155                 160                 165

gtt cgt aat ctt gga ctt act cca atg gat caa gga tca ctc atg gca          639
Val Arg Asn Leu Gly Leu Thr Pro Met Asp Gln Gly Ser Leu Met Ala
170                 175                 180                 185

gcc aaa gaa att gaa aag tac ccc ctg cag cta ttt cca atg tgg agg          687
Ala Lys Glu Ile Glu Lys Tyr Pro Leu Gln Leu Phe Pro Met Trp Arg
                190                 195                 200

ttc ccc ttc tat ttg tct gct gtg ctg tgt gtc ttc ttg ttt ttc tat          735
Phe Pro Phe Tyr Leu Ser Ala Val Leu Cys Val Phe Leu Phe Phe Tyr
            205                 210                 215

tgt gtt ata aga gac gta atc tac cct tat gtt tat gaa aag aaa gat          783
Cys Val Ile Arg Asp Val Ile Tyr Pro Tyr Val Tyr Glu Lys Lys Asp
        220                 225                 230

aat aca ttt cgt atg gct att tcc att cca aat cgt atc ttt cca ata          831
Asn Thr Phe Arg Met Ala Ile Ser Ile Pro Asn Arg Ile Phe Pro Ile
        235                 240                 245

aca gca ctt aca ctg ctt gct ttg gtt tac ctc cct ggt gtt att gct          879
Thr Ala Leu Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Val Ile Ala
250                 255                 260                 265

gcc att cta caa ctg tac cga ggc aca aaa tac cgt cga ttc cca gac          927
Ala Ile Leu Gln Leu Tyr Arg Gly Thr Lys Tyr Arg Arg Phe Pro Asp
                270                 275                 280

tgg ctt gac cac tgg atg ctt tgc cga aag cag ctt ggc ttg gta gct          975
Trp Leu Asp His Trp Met Leu Cys Arg Lys Gln Leu Gly Leu Val Ala
            285                 290                 295

ctg gga ttt gcc ttc ctt cat gtc ctc tac aca ctt gtg att cct att          1023
Leu Gly Phe Ala Phe Leu His Val Leu Tyr Thr Leu Val Ile Pro Ile
            300                 305                 310

cga tat tat gta cga tgg aga ttg gga aac tta acc gtt acc cag gca          1071
Arg Tyr Tyr Val Arg Trp Arg Leu Gly Asn Leu Thr Val Thr Gln Ala
        315                 320                 325

ata ctc aag aag gag aat cca ttt agc acc tcc tca gcc tgg ctc agt          1119
Ile Leu Lys Lys Glu Asn Pro Phe Ser Thr Ser Ser Ala Trp Leu Ser
330                 335                 340                 345

gat tca tat gtg gct ttg gga ata ctt ggg ttt ttt ctg ttt gta ctc          1167
Asp Ser Tyr Val Ala Leu Gly Ile Leu Gly Phe Phe Leu Phe Val Leu
            350                 355                 360
```

```
ttg gga atc act tct ttg cca tct gtt agc aat gca gtc aac tgg aga    1215
Leu Gly Ile Thr Ser Leu Pro Ser Val Ser Asn Ala Val Asn Trp Arg
            365                 370                 375

gag ttc cga ttt gtc cag tcc aaa ctg ggt tat ttg acc ctg atc ttg    1263
Glu Phe Arg Phe Val Gln Ser Lys Leu Gly Tyr Leu Thr Leu Ile Leu
        380                 385                 390

tgt aca gcc cac acc ctg gtg tac ggt ggg aag aga ttc ctc agc cct    1311
Cys Thr Ala His Thr Leu Val Tyr Gly Gly Lys Arg Phe Leu Ser Pro
        395                 400                 405

tca aat ctc aga tgg tat ctt cct gca gcc tac gtg tta ggg ctt atc    1359
Ser Asn Leu Arg Trp Tyr Leu Pro Ala Ala Tyr Val Leu Gly Leu Ile
410                 415                 420                 425

att cct tgc act gtg ctg gtg atc aag ttt gtc cta atc atg cca tgt    1407
Ile Pro Cys Thr Val Leu Val Ile Lys Phe Val Leu Ile Met Pro Cys
                430                 435                 440

gta gac aac acc ctt aca agg atc cgc cag ggc tgg gaa agg aac tca    1455
Val Asp Asn Thr Leu Thr Arg Ile Arg Gln Gly Trp Glu Arg Asn Ser
                445                 450                 455

aaa cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt            1504
Lys His  *
```

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caatttagct ggatttctga actatggttt tgaatgttta aagaagaatg atgggtacag    1564
ttaggaaagt ttttttctta caccgtgact gagggaaaca ttgcttgtct ttgagaaatt    1624
gactgacata ctggaagaga acaccatttt atctcaggtt agtgaagaat cagtgcaggt    1684
ccctgactct tattttccca gaggccatgg agctgagatt gagactagcc ttgtggtttc    1744
acactaaaga gtttccttgt tatgggcaac atgcatgacc taatgtcttg caaaatccaa    1804
tagaagtatt gcagcttcct tctctggctc aagggctgag ttaagtgaaa ggaaaaacag    1864
cacaatggtg accactgata aaggctttat taggtatatc tgaggaagtg ggtcacatga    1924
aatgtaaaaa gggaatgagg tttttgttgt tttttggaag taaaggcaaa cataaatatt    1984
accatgatga attctagtga aatgacccct tgactttgct tttcttaata cagatattta    2044
ctgagaggaa ctattttat aacacaagaa aaatttacaa ttgattaaaa gtatccatgt    2104
cttggataca tacgtatcta tagagctggc atgtaattct tcctctataa agaataggta    2164
taggaaagac tgaataaaaa tggagggata tccccttgga tttcacttgc attgtgcaat    2224
aagcaaagaa gggttgataa aagttcttga tcaaaaagtt caaagaaacc agaattttag    2284
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tttctcaaat ccttgctgaa atttaggatg gttctcactg tttttctgtg ctgatagtac    2644
cctttccaag gtgaccttca gggggattaa ccttcctagc tcaagcaatg agctaaaagg    2704
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tgagacagtc ttgctctgtc gctcaggctg gagtgcagtg cacgatctc agctcactgc    3064
aacctcctcc tcccaggttc aagtgattct tgttcatcag cctcccgagt agctgggact    3124
acaggcatgt gccactatgc ccagctaatt tttgtacttt tagtagagac agggtttcac    3184
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11

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cacattggtc aggctggtct tgaaatgctg gcgtcaagtg atctgcctgc ctccgcctta    3244
cgtaatatat tttcttaatg gctgcataat atcacatcaa ataggcattt ttcaaacctc    3304
tttccttatt aaacatgtag actatatcca tttttacta aaataaataa catttcagat     3364
aatatctttg cactgataat gttgccaagc catttctaaa gtgaccttat caatttaatt    3424
accattggat gagggtgttg ctttcatcgc accattgtag attgtctttt ttatttcaat    3484
ttgcgtttat ttataactgg ttgcaaaggt acacagaaca cacgctcctt caactatct     3544
ttgataaacc caagcaagga tacaaaaagt tggacgacat tgagtagagt catggtatac    3604
ggtgctgacc ctacagtatc agtggaaaag ataaggaaaa tgtcactact cacctatgtt    3664
atgcaaaaca gttaggtgtg ctggggctgg atactgctct tttacttgag cattggttga    3724
ttaaagttta ggtaccatcc aggctggtct agagaagtct ttggagttaa ccatgctctt    3784
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aatgccatcc ataggtaaaa tgctgaccta tagaaaaaaa tgaactctac ttttatagcc    3904
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agtgctccaa gccccaccag ctgaccaaag aaagcccaag ttctccttct gtccttccca    4084
caacctccct gctcccaaaa ctatgaaatt aatttgacca tattaacaca gctgactcct    4144
ccagtttact taaggtagaa agaatgagtt tacaacagat gaaaataagt gctttgggcg    4204
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<210> 8
<211> 459
<212> PRT
<213> Homo sapiens

<400> 8
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Met Glu Lys Thr Cys Ile Asp Ala Leu Pro Leu Thr Met Asn Ser Ser
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Glu Lys Gln Glu Thr Val Cys Ile Phe Gly Thr Gly Asp Phe Gly Arg
             20              25              30
Ser Leu Gly Leu Lys Met Leu Gln Cys Gly Tyr Ser Val Val Phe Gly
         35              40              45
Ser Arg Asn Pro Gln Lys Thr Thr Leu Leu Pro Ser Gly Ala Glu Val
     50              55              60
Leu Ser Tyr Ser Glu Ala Ala Lys Lys Ser Gly Ile Ile Ile Ala
65                  70              75              80
Ile His Arg Glu His Tyr Asp Phe Leu Thr Glu Leu Thr Glu Val Leu
             85                  90              95
Asn Gly Lys Ile Leu Val Asp Ile Ser Asn Asn Leu Lys Ile Asn Gln
             100             105             110
Tyr Pro Glu Ser Asn Ala Glu Tyr Leu Ala His Leu Val Pro Gly Ala
         115             120             125
His Val Val Lys Ala Phe Asn Thr Ile Ser Ala Trp Ala Leu Gln Ser
    130                 135             140
Gly Ala Leu Asp Ala Ser Arg Gln Val Phe Val Cys Gly Asn Asp Ser
145             150             155             160
Lys Ala Lys Gln Arg Val Met Asp Ile Val Arg Asn Leu Gly Leu Thr
             165             170             175
Pro Met Asp Gln Gly Ser Leu Met Ala Ala Lys Glu Ile Glu Lys Tyr
             180             185             190
Pro Leu Gln Leu Phe Pro Met Trp Arg Phe Pro Phe Tyr Leu Ser Ala
         195             200             205
Val Leu Cys Val Phe Leu Phe Phe Tyr Cys Val Ile Arg Asp Val Ile
    210             215                 220
Tyr Pro Tyr Val Tyr Glu Lys Lys Asp Asn Thr Phe Arg Met Ala Ile
```

12
```

Ser Ile Pro Asn Arg Ile Phe Pro Ile Thr Ala Leu Thr Leu Leu Ala
                245                 250                 255
Leu Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Leu Gln Leu Tyr Arg
            260                 265                 270
Gly Thr Lys Tyr Arg Arg Phe Pro Asp Trp Leu Asp His Trp Met Leu
            275                 280                 285
Cys Arg Lys Gln Leu Gly Leu Val Ala Leu Gly Phe Ala Phe Leu His
        290                 295                 300
Val Leu Tyr Thr Leu Val Ile Pro Ile Arg Tyr Tyr Val Arg Trp Arg
305                 310                 315                 320
Leu Gly Asn Leu Thr Val Thr Gln Ala Ile Leu Lys Lys Glu Asn Pro
                325                 330                 335
Phe Ser Thr Ser Ser Ala Trp Leu Ser Asp Ser Tyr Val Ala Leu Gly
            340                 345                 350
Ile Leu Gly Phe Phe Leu Phe Val Leu Leu Gly Ile Thr Ser Leu Pro
            355                 360                 365
Ser Val Ser Asn Ala Val Asn Trp Arg Glu Phe Arg Phe Val Gln Ser
        370                 375                 380
Lys Leu Gly Tyr Leu Thr Leu Ile Leu Cys Thr Ala His Thr Leu Val
385                 390                 395                 400
Tyr Gly Gly Lys Arg Phe Leu Ser Pro Ser Asn Leu Arg Trp Tyr Leu
                405                 410                 415
Pro Ala Ala Tyr Val Leu Gly Leu Ile Ile Pro Cys Thr Val Leu Val
            420                 425                 430
Ile Lys Phe Val Leu Ile Met Pro Cys Val Asp Asn Thr Leu Thr Arg
        435                 440                 445
Ile Arg Gln Gly Trp Glu Arg Asn Ser Lys His
    450                 455

<210> 9
<211> 322
<212> DNA
<213> Homo sapiens

<400> 9
ggtcgacttt tcctttattc ctttgtcaga gatctgattc atccatatgc tagaaaccaa      60
cagagtgact tttacaaaat tcctatagag attgtgaata aaaccttacc tatagttgcc     120
attactttgc tctccctagt ataccttgca ggtcttctgg cagctgctta tcaactttat     180
tacggcacca agtataggag atttccacct tggttggaaa cctggttaca gtgtagaaaa     240
cagcttggat tactaagttg tttcttcgct atggtccatg ttgcctacag cctctgctta     300
ccgatgagaa ggtcagagag at                                              322

<210> 10
<211> 183
<212> DNA
<213> Homo sapiens

<400> 10
tttgcagctt tgcagatacc cagactgagc tggaactgga atttgtcttc ctattgactc      60
tacttcttta aaagcggctg cccattacat tcctcagctg tccttgcagt taggtgtaca     120
tgtgactgag tgttggccag tgagatgaag tctcctcaaa ggaaggcagc atgtgtcctt     180
ttt                                                                   183

<210> 11
<211> 448
<212> DNA

13

<213> Homo sapiens

<400> 11
aagaaggaga atccatttag cacctcctca gcctggctca gtgattcata tgtggctttg       60
ggaatacttg ggtttttct gtttgtactc ttgggaatca cttctttgcc atctgttagc       120
aatgcagtca actggagaga gttccgattt gtccagtcca aactgggtta tttgaccctg       180
atcttgtgta cagcccacac cctggtgtac ggtgggaaga gattcctcag cccttcaaat       240
ctcagatggt atcttcctgc agcctacgtg ttagggctta tcattccttg cactgtgctg       300
gtgatcaagt ttgtcctaat catgccatgt gtagacaaca cccttacaag gatccgccag       360
ggctgggaaa ggaactcaaa acactagaaa aagcattgaa tggaaaatca atatttaaaa       420
caaagttcaa tttagctgga aaaaaaaa                                          448


<210> 12
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 11,56,233,250,310,326,377,398
<223> n=a, t, c, or g

<400> 12
ggccgcggca nccgctacga cctggtcaac ctggcagtca agcaggtctt ggccanacaa       60
gagccacctc tgggtgaagg aggaggtctg gcggatggag atctacctct ccctgggagt       120
gctggccctc ggcacgttgt ccctgctggc cgtgacctca ctgccgtcca ttgcaaactc       180
gctcaactgg agggagttca gcttcgttca gtcctcactg ggctttgtgg ccntcgtgct       240
gagcacactn cacacgctca cctacggctg acccgcgcc ttcgaggaga gccgctacaa       300
gttctacctn cctcccacct tcacgntcac gctgctggtg ccctgcgttc gttcatcctg       360
ggccaaagcc ctgtttntac tgccttgcat tcagccgnag a                          401


<210> 13
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<223> Xaa = Any amino acid

<400> 13
Ala Ala Ala Xaa Ala Thr Thr Trp Ser Thr Trp Gln Ser Ser Arg Ser
1               5                   10                  15
Trp Pro Xaa Lys Ser His Leu Trp Val Lys Glu Glu Val Trp Arg Met
            20                  25                  30
Glu Ile Tyr Leu Ser Leu Gly Val Leu Ala Leu Gly Thr Leu Ser Leu
            35                  40                  45
Leu Ala Val Thr Ser Leu Pro Ser Ile Ala Asn Ser Leu Asn Trp Arg
        50                  55                  60
Glu Phe Ser Phe Val Gln Ser Ser Leu Gly Phe Val Ala Xaa Val Leu
65                  70                  75                  80
Ser Thr Leu His Thr Leu Thr Tyr Gly Trp Thr Arg Ala Phe Glu Glu
                85                  90                  95
Ser Arg Tyr Lys Phe Tyr Leu Pro Pro Thr Phe Thr Xaa Thr Leu Leu
            100                 105                 110
Val Pro Cys Val Arg Ser Ser Trp Ala Lys Ala Leu Phe Xaa Leu Pro
            115                 120                 125
Cys Ile Gln Pro Xaa

14

130

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
actttgttga tgaccaggat tgga                                        24

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
cagaacttca gcacacacag gaac                                        24

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
ttaggacaac ttgatcacca gca                                         23

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 17
tgtccagtcc aaactgggtt attt                                        24

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
agggagttca gcttcgttca gtc                                         23

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
ggtagaactt gtagcggctc tcct                                          24

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
gactgagctg gaactggaat ttgt                                          24

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 21
tttgaggaga cttcatctca ctgg                                          24

<210> 22
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 22
ttttgtacaa gctt                                                     14

<210> 23
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 23
ctaatacgac tcactatagg gctcgagcgg ccgcccgggc aggt                    44

<210> 24
<211> 10

<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 24
ggcccgtcca                                                              10

<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 25
gtaatacgac tcactatagg gcagcgtggt cgcggccgag gt                          42

<210> 26
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> adaptor

<400> 26
cggctcca                                                                8

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27
ctaatacgac tcactatagg gc                                                22

<210> 28
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28
tcgagcggcc gcccgggcag gt                                                22

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
agcgtggtcg cggccgaggt                                                    20

<210> 30
<211> 15
<212> PRT
<213> Homo sapiens

<400> 30
Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp Ile Glu His
1               5                   10                  15

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31
gactgagctg gaactggaat ttgt                                               24

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
tttgaggaga cttcatctca ctgg                                               24

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 33
acaagagcca cctctgggtg aa                                                 22

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 34

agttgagcga gtttgcaatg gac 23